

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

## Kaushal, Sumesh

---

From: Kaushal, Sumesh  
Sent: Tuesday, February 25, 2003 4:13 PM  
To: STIC-ILL  
Subject: ref-req#09297181

TI Restoration of transcriptional activity of p53 mutants in human tumour cells by intracellular expression of anti-p53 single chain Fv fragments.

SO ONCOGENE, (1999 Jan 14) 18 (2) 551-7.

Journal code: 8711562. ISSN: 0950-9232.

AU Caron de Fromentel C; Gruel N; Venot C; Debussche L; Conseiller E; Dureau C; Teillaud J L; Tocque B; Bracco L

TI A tumor specific single chain antibody dependent gene expression system.

SO ONCOGENE, (1999 Jan 14) 18 (2) 559-64.

Journal code: 8711562. ISSN: 0950-9232.

AU Mary M N; Venot C; Caron de Fromentel C; Debussche L; Conseiller E; Cochet O; Gruel N; Teillaud J L; Schweighoffer F; Tocque B; Bracco L

TI Mutations in p53 produce a common conformational effect that can be detected with a panel of monoclonal antibodies directed toward the central part of the p53 protein

SO **Oncogene** (1994), 9(12), 3689-94

CODEN: ONCNES; ISSN: 0950-9232

TI Antibody fragments from a 'single pot' phage display library as immunochemical reagents:

SO EMBO JOURNAL, (1994 Feb 1) 13 (3) 692-8.

Journal code: 8208664. ISSN: 0261-4189.

AU Nissim A; Hoogenboom H R; Tomlinson I M; Flynn G; Midgley C; Lane D; Winter G

TI Characterization of scFv-421, a single-chain antibody targeted to p53.

SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Jan 13) 230 (2) 242-6.

Journal code: 0372516. ISSN: 0006-291X.

AU Jannot C B; Hynes N E

*S. Kaushal*

CM1 12A07 AU1636

Ph: 703-305-6838

Mail Box: 11E12



## SHORT REPORT

# A tumor specific single chain antibody dependent gene expression system

Marie-Noëlle Mary<sup>1</sup>, Corinne Venot<sup>1</sup>, Claude Caron de Fromental<sup>1,4</sup>, Laurent Debussche<sup>1</sup>, Emmanuel Conseiller<sup>1</sup>, Olivier Cochet<sup>2,5</sup>, Nadège Gruel<sup>2</sup>, Jean-Luc Teillaud<sup>2,3</sup>, Fabien Schweighoffer<sup>1,5</sup>, Bruno Tocque<sup>1,5</sup> and Laurent Bracco<sup>1,5</sup>

<sup>1</sup>Gene Medicine Department, Rhône-Poulenc Rorer S.A., 13 quai Jules Guesde, 94403 Vitry-sur-Seine, France; <sup>2</sup>Laboratoire de Biotechnologie des Anticorps; <sup>3</sup>Institut Curie, Unité INSERM 255, 26 rue d'Ulm, 75005 Paris, France

The design of conditional gene expression systems restricted to given tissues or cellular types is an important issue of gene therapy. Systems based on the targeting of molecules characteristic of the pathological state of tissues would be of interest. We have developed a synthetic transcription factor by fusing a single chain antibody (scFv) directed against p53 with the bacterial tetracycline repressor as a DNA binding domain. This hybrid protein binds to p53 and can interact with a synthetic promoter containing tetracycline-operator sequences. Gene expression can now be specifically achieved in tumor cells harboring an endogenous mutant p53 but not in a wild-type p53 containing tumor cell line or in a non-transformed cell line. Thus, a functional transactivator centered on single chain antibodies can be expressed intracellularly and induce gene expression in a scFv-mediated specific manner. This novel class of transcriptional transactivators could be referred as 'trabodies' for transcription-activating-antibodies. The trabodies technology could be useful to any cell type in which a disease related protein could be the target of specific antibodies.

**Keywords:** gene expression; gene therapy; scFv; p53

The possibility to restrain the function of a therapeutic gene in a given cell type or tissue may be a critical issue in the field of gene therapy. Viral and non viral vectors that would carry such a therapeutic gene may be engineered to target a specific cell type. Thus, ligands have been introduced into the envelope of viral vectors to bind their cognate receptors specifically expressed at the surface of the target cells (Nilson *et al.*, 1996). Specificity could also be achieved at the level of gene expression. Most efforts have focused at the transcriptional level through the use of tissue specific promoters derived from genes, which have a restricted expression pattern (Ayoubi and Van De Ven 1996). Another approach would be to design a restricted gene expression system based on the targeting of disease-related molecules whose expression and functional activity is a landmark of the pathological state. For

instance, oncogenes and tumor suppressor genes represent specific markers of cancer cells through overexpression, mutation or deletion. It would be advantageous to use such marker molecules as the basis of a restricted gene expression system. We decided to design a specific gene expression system by choosing p53 mutant as a target model. p53 represents the most frequent genetic alteration in human cancers (Hainaut *et al.*, 1997). Ninety percent of these alterations are missense mutations, which for the most part induce a conformational change leading to a stabilization of the protein, preventing DNA binding and subsequent transcriptional activation (Hainaut *et al.*, 1997; Harris, 1993). Such missense mutations occur within the core of p53, leaving the amino-terminal transactivation domain intact. If this transactivation domain could be recruited to activate a synthetic promoter, one could reasonably hope to achieve p53 mutant specific gene expression. Such an approach is reminiscent of the double hybrid system, originally described in yeast and which has also been applied to mammalian cells (Fields and Sternglanz, 1994; Luo *et al.*, 1997). In this approach, it is absolutely required to use a known ligand for the target to be recruited. As p53 form tetramers via a carboxy-terminal domain, one could envision to use this oligomerization domain. In addition, p53 specific partners could be the basis for defining domains that would serve as ligands as well. However, ligands specific for a chosen target are not always available. Thus, we tried to develop a system centred on a type of universal ligand. Monoclonal antibodies or their fragments (Fab', Fv) would in principle represent such ligands. They can display high specificity with excellent affinities. Single chain Fv antibody fragment (scFv) in which the variable light and heavy chains are connected via a flexible linker and expressed as a single polypeptide represent the smallest functional fragment that maintain binding and specificity (Huston *et al.*, 1988; Glockshuber *et al.*, 1990). Several applications of intracellular expression of scFv's have been reported, defining them as a potential new class of therapeutic reagents (Richardson and Marasco, 1995). HIV viral proteins such as tat, rev, gp120 (Pilkington *et al.*, 1996; Chen *et al.*, 1996), oncogene products such as Ras (Biocca *et al.*, 1994; Cochet *et al.*, 1998), *erbB-2* (Schmidt *et al.*, 1996), EGF receptors (Jannot *et al.*, 1996) and other membrane receptors such as IL2-R (Richardson *et al.*, 1995) have been the targets of scFv's which inhibited their function sometimes by redirecting their localization in another cellular compartment (Persic *et al.*, 1997a). Several examples of chimeric proteins joining scFv's to

Correspondence: L Bracco

Current addresses: <sup>4</sup>Unité INSERM 380, Institute Cochin de Génétique Moléculaire, 22 rue Méchain, 75014 Paris, France; <sup>5</sup>ExonHit Therapeutics SA, 65 Boulevard Masséna, 75013 Paris, France

Received 30 May 1998; revised 20 August 1998; accepted 20 August 1998

other functional moieties such as toxins (Wels *et al.*, 1995), dimerization domains (de Kruif and Logtenberg, 1996; Hu *et al.*, 1996), TCR CD3 z-chain (Moritz and Groner, 1995), protamine (Chen *et al.*, 1995) have also been described. These chimeras rely on the scFv to work as a specific ligand. Here, we assign transcriptional activation as a novel application for scFv based chimeric molecules, which is exemplified by the fusion between an anti-p53 scFv and the bacterial tetracycline repressor as a DNA binding motif (Figure 1). A single chain Fv fragment was derived from the anti-p53 PAb421 monoclonal antibody (Caron de Fromentel *et*

*al.* accompanying manuscript). PAb421 recognizes an epitope localized in the carboxy-terminal domain of p53 (Arai *et al.*, 1986). Thus, recruitment of an endogenous mutant p53 by the pAb421-derived scFv should not interfere with its transactivation domain, which is located within the amino-terminal moiety. Although pAb421 cannot discriminate between wild-type and mutant p53, we assumed that the increased half-life of mutant p53 compared to wild-type p53 (Reihnsaus *et al.*, 1990) would nevertheless result in a mutant p53 specific effect. The 421-ScFv was cloned by phage display and was shown to bind to p53 (Caron de Fromentel *et al.* accompanying manuscript; Figure 2). We chose the tetracycline repressor (TetR) as a specific DNA binding unit for the following reasons. The DNA operator sequences recognized by tetR are 17 base pair long rendering very unlikely the existence of such sequences within the human genome. In addition, the TetR has been successfully used as a fusion protein with the VP16 activation domain, constituting the basis of a pharmacologically regulated gene expression system *in vitro* and *in vivo* (Gossen and Bujard, 1992;

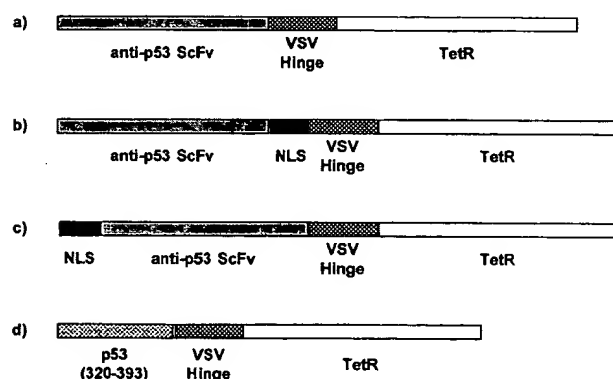


Figure 1 Schematic representation of the chimeric transcription factors. The anti-p53 pAb421 ScFv with or without nuclear localisation signal (NLS) (a,b,c) or the p53 oligomerization domain (320-393) (d) were fused to the tetracycline repressor via the VSV-Hinge linker

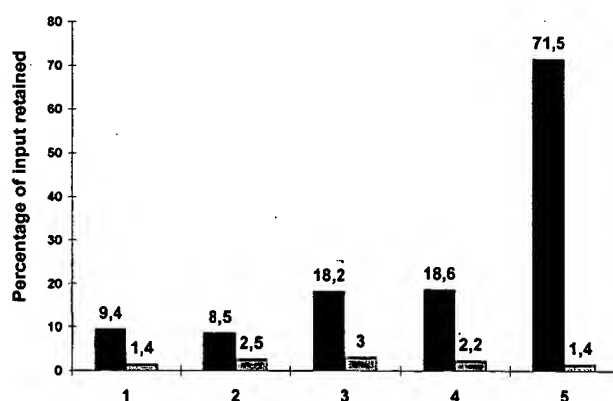


Figure 2 Co-immunoprecipitation assays between the TetR-chimeras and p53. The various constructs were produced and <sup>35</sup>S-labelled *in vitro* from pCDNA3 derived vectors (TnT kit, Promega). Equimolar amounts of the translated products were then incubated with either 1 mg of unlabeled full length p53 (1-393, black boxes) or 0.8 mg of unlabeled deleted p53 (p53Δ320-393, grey boxes) produced and purified from Baculovirus nuclear extracts in 10 mM Tris.HCl (pH 8.0), 1 mM EDTA, 150 mM NaCl, 1% NP-40. The reaction samples were immunoprecipitated with DO-1 using Immunoprecipitin (Gibco-BRL) as a carrier, washed and eluted. The immunoprecipitates were analyzed via polyacrylamide gel electrophoresis and quantified with an Instant Imager (Packard Instruments). Quantification of the amount of the immunoprecipitated complexes obtained with full length p53 (black boxes) or a truncated p53 deleted in its carboxy-terminal (1-320) (grey boxes) are reported as a percentage with respect to the labelled input. 1: Naked pAb421 ScFv, 2: ScFv/TetR, 3: NLS-ScFv/TetR, 4: ScFv-NLS/TetR, 5: (320-393)/TetR

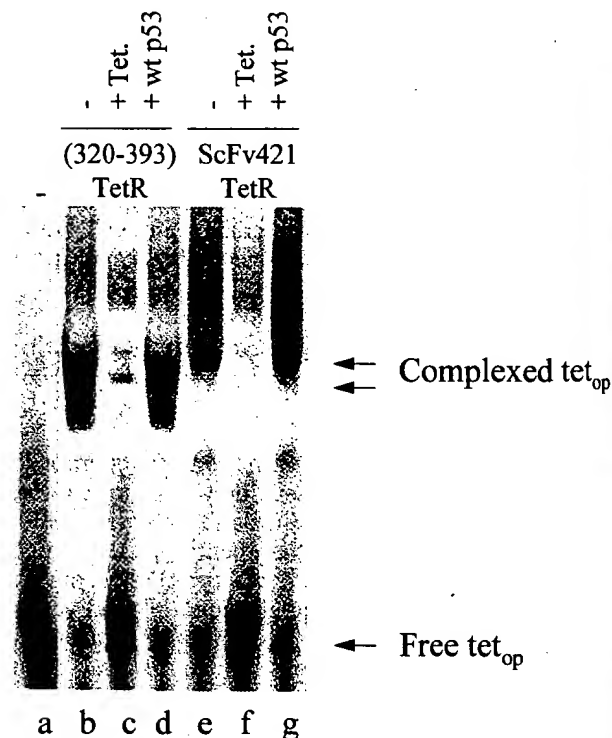


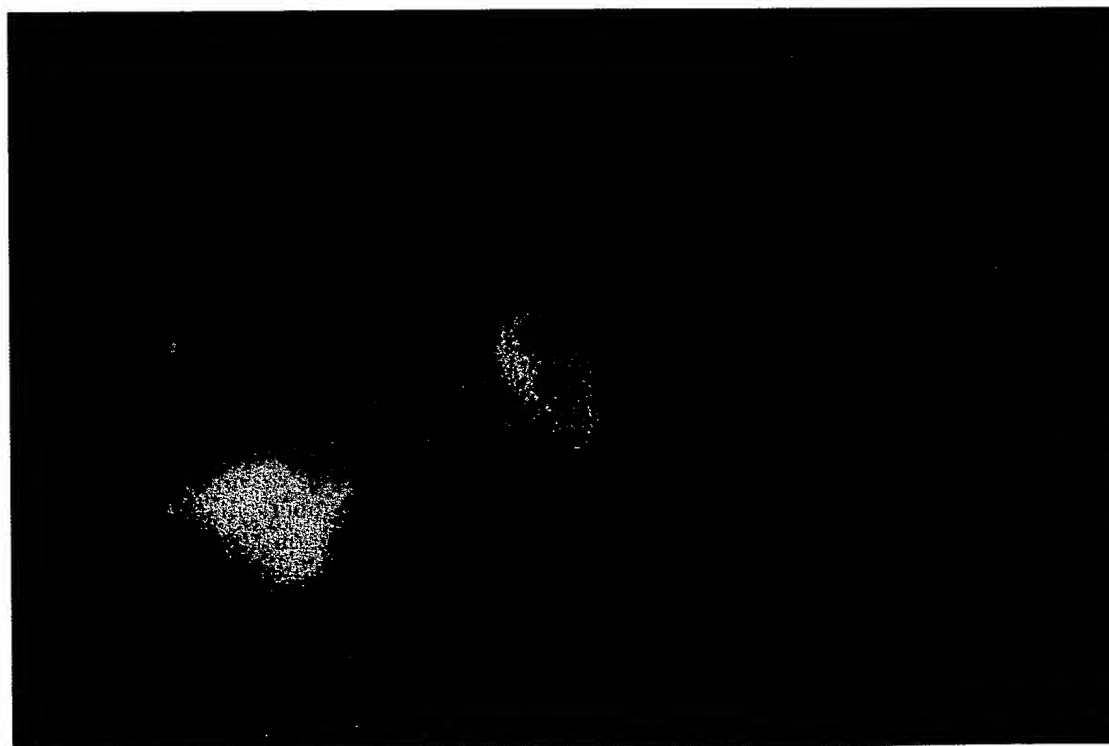
Figure 3 Gel retardation assays between the tetR-chimeras and a tet operator containing ds DNA. A synthetic double-stranded oligonucleotide corresponding to the tetracycline operator sequence was labeled with <sup>32</sup>P-ATP and T4 polynucleotide kinase. The (320-393)/TetR and ScFv/TetR and ScFv/TetR were produced unlabelled *in vitro* as above-described. The operator DNA (10<sup>-10</sup> M) and the translated products were incubated for 15 min at room temperature in 10 mM Tris.HCl (pH 7.4), 10 mM MgCl<sub>2</sub>, 10 mM KCl, 6 mM beta-mercaptoethanol, 0.1 mM EDTA, 0.5 mg/ml BSA, 10<sup>-8</sup> M competitor AP2 DNA. The samples were resolved on a 5% acrylamide gel. When required, tetracycline (10 mM) or purified p53 (100 ng) were pre-incubated with the translated products before adding the labeled operator DNA. (320-393)/TetR and ScFv/TetR were incubated with a 20 base pair DNA element containing the tet operator (lanes b,e). Before adding the tet operator DNA, the two chimeras were incubated with tetracycline (lanes c,f) or wild-type p53 (lanes d,g)

Kistner *et al.*, 1996). The 421-ScFv was positioned as an amino-terminal fusion with the TetR (ScFv/TetR, Figure 1a). Fusion molecules containing scFv's have been realized in this orientation and allow proper recognition of the antigen (Kistner *et al.*, 1996). In addition, the fused moiety may stabilize the scFv, substituting to some extent to the immunoglobulin light chain constant region (Mhashilkar *et al.*, 1995). A linker, VSV-Hinge, including a ten aminoacid long peptide derived from the upper hinge region of mouse IgG3 (Pack and Pluckthun, 1992) and an immunodetectable tag consisting of a 11 amino-acid long peptide derived from the carboxy-terminal domain of the Vesicular Stomatitis Virus glycoprotein (Kreis, 1986) was inserted between the scFv and the TetR. In addition, a nuclear localization signal derived from the SV40 Large T antigen (NLS) (Goldfarb *et al.*, 1986) was included at the amino-terminal or carboxy-terminal end of the scFv in the chimera (NLS-ScFv/TetR and ScFv-NLS/TetR, Figure 1b and c). The p53 oligomerization domain corresponding to amino-acids 320-393 was used as a positive control ((320-393)/TetR, Figure 1d) as this domain was previously shown to properly fold and oligomerize with p53 when expressed intracellularly alone or fused to the DNA binding domain of the Gal4 yeast transactivator (Shaulian *et al.*, 1992; Da Costa *et al.*, 1996).

Co-immunoprecipitation assays were performed to determine whether the fused scFv maintained its ability to recognize p53 when expressed as a chimera. The various chimeras and the naked scFv as a control were <sup>35</sup>S-labelled in an *in vitro* synthesis using rabbit

reticulocyte lysates. They were incubated with either unlabelled full-length wild-type p53 or with an unlabelled carboxy-terminally truncated p53 (p53Δ320-393) which served as a negative control since it lacks the p53 oligomerization domain and the pAb421 epitope. The complexes were immunoprecipitated with DO1, a monoclonal antibody directed against the p53 amino-terminal domain which binds the full-length and the truncated p53 proteins equally well. The amount of co-immunoprecipitated labeled material was evaluated following gel electrophoresis (Figure 2). The scFv's present in the various chimeras were able to specifically recognize p53 via its carboxy-terminal epitope. The fusion molecules bearing the NLS seemed more efficient in binding p53 which may be due to a better folding of the scFv. However, the ScFv/TetR proteins appeared to be less efficient in associating with p53 than (320-393)/TetR suggesting that the oligomerization domain displays a stronger affinity for p53 than the 421-ScFv.

The functionality of the TetR as a specific DNA binding motif within the chimeras was tested in a gel retardation assay. <sup>32</sup>P-labelled Tet operator DNA was incubated with unlabelled ScFv/TetR and (320-393)/TetR produced from reticulocyte lysates. Retarded bands were obtained with both chimeras (Figure 3b and e). These signals were TetR-dependent as they were displaced upon the addition of tetracycline (Figure 3c and f). Incubating purified wild-type p53 with the chimeras before adding the operator DNA did not prevent the formation of the retarded complex (Figure 3d and g), suggesting a lack of steric hindrance

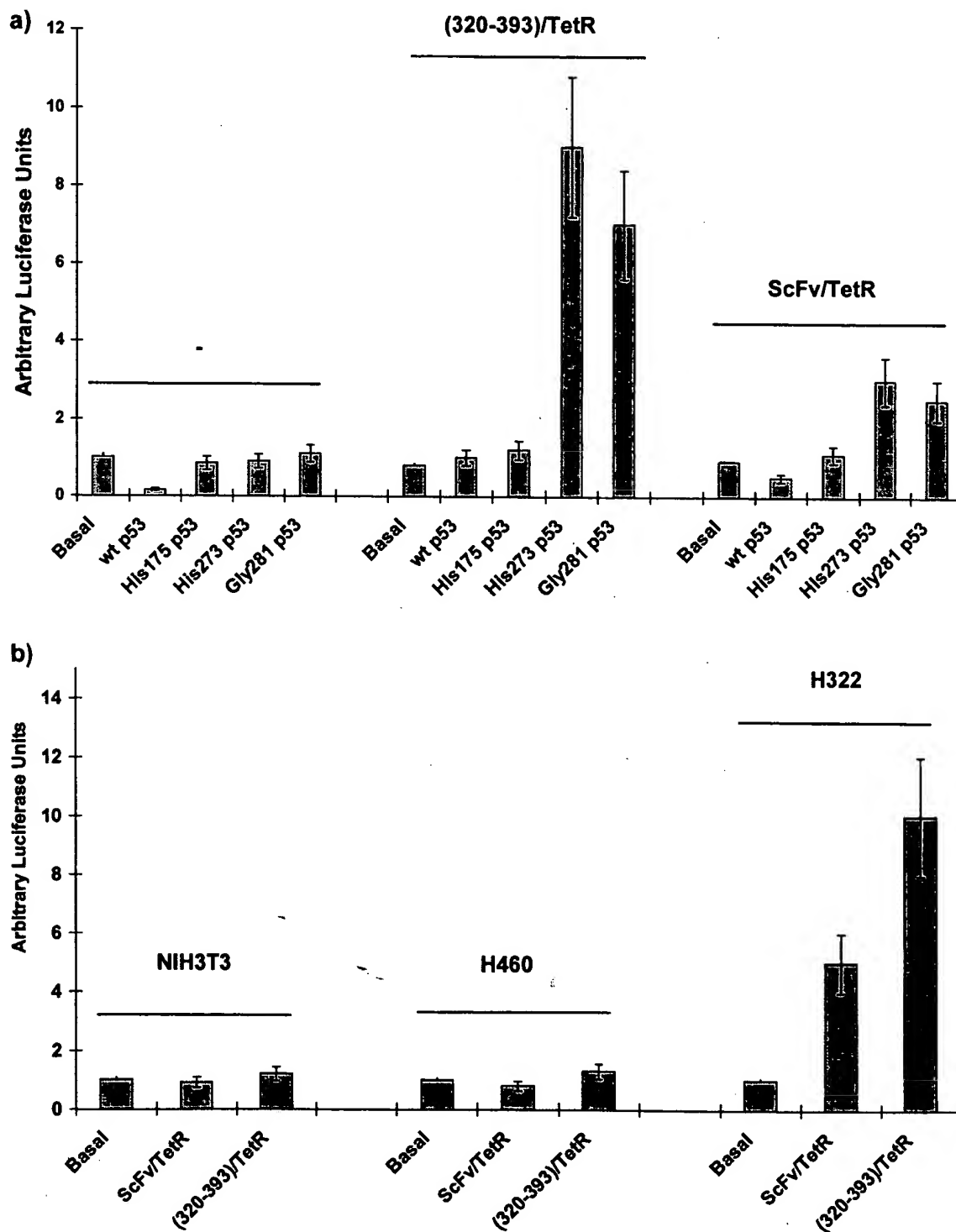


**Figure 4** Nuclear staining of the ScFv/TetR fusion protein in H1299 cells. A rabbit polyclonal antibody was raised against four different ScFvs purified from *E. coli* periplasmic fractions. This polyclonal was shown to recognize separate ScFvs as well as total IgGs (Cochet *et al.*, 1998). Upon plating on culture chambers (Lab-Tek, Nunc), H1299 cells were transfected with control or expression vector for scFv/TetR. Twenty-four hours later, cells were fixed in PBS/formaldehyde 4%, permeabilized in PBS/Triton X-100 0.2% then incubated with the anti-ScFv antibody in Power Block buffer (BioGenex) to be revealed with a secondary anti-rabbit IgG serum coupled to FITC (Jackson ImmunoResearch). Upon transfection of the ScFv/TetR expression vector in H1299 cells, a nuclear localization was observed in every transfected cell, as revealed with an anti-scFv polyclonal antibody

between bound p53 and TetR. Similar data were obtained with the NLS containing chimeras (data not shown).

As we had evidence that both moieties, the scFv and the TetR were functional within the chimeras, we

pursued the evaluation of these hybrid proteins following expression in mammalian cells. Following transient transfection in H1299, a p53 null lung carcinoma cell line, protein expression and localization were monitored using a rabbit anti-ScFv polyclonal



**Figure 5** Transactivating functions of the two tetR-chimeras. Transient transfection assays were performed using Lipofectamine (Gibco-BRL) and a DNA compacting Histone H1-derived peptide (Byk *et al.*, 1995). pUHC13-6 bearing the luciferase reporter gene under the control of a tetracycline-dependent promoter (Gossen and Bujard, 1992) was used in each assay. The luciferase activity was quantified 48 h after transfection (Luciferase Assay System, Promega). Data are expressed as the mean of three independent experiments. (a) Transient transfections in H358 (p53 null) cell line. Expression vectors for wt or mutant p53 (500 ng), for (320-393)/TetR or ScFv/TetR (250 ng) and for the appropriate luciferase reporter gene (250 ng) were introduced in H358. The basal signal has been set to one arbitrary unit. (b) Transient transfections in NIH3T3, H460 and H322 cell lines. Expression vectors for (320-393)/TetR or ScFv/TetR (250 ng) and the luciferase reporter gene (250 ng) were introduced in the various cell lines. The basal signal has been set to one arbitrary unit, independently in each cell line

antiseru  
with S  
potenti  
the cor  
observe  
consen  
Wester  
at the  
shown  
nucleu  
transcr  
chimer  
well (c

The  
mediat  
transie  
was pl  
downs  
quenc  
expres  
witho  
His27  
null 1  
repres  
exerte  
(Gins  
reliev  
level  
Coex  
and  
muta  
resul  
His1  
(Fiel  
obtai  
cules  
nopr  
effici  
of tl  
obta  
next  
in a  
expr  
repc  
(320  
in tl  
the  
cell  
by  
NIH  
chir  
the  
exp  
this  
as  
exc  
ger

Re:

Ar

Ay

proteins  
following  
null lung  
localization  
polyclonal

antiserum. Strong nuclear fluorescence was observed with ScFv/TetR (Figure 4) although no obvious potential NLS sequences seem to be present within the construct. A similar nuclear localization has been observed for Tet/VP16 which does not contain any consensus NLS sequences as well (Kistner *et al.*, 1996). Western blotting revealed the expression of ScFv/TetR at the proper apparent molecular weight (data not shown). ScFv/TetR can therefore localize into the nucleus, a prerequisite for its efficient function as a transcriptional transactivator. The NLS containing chimeras displayed a strong nuclear localization as well (data not shown).

The ability of the chimeric transcription factors to mediate mutant p53 gene expression was assessed in transient transfection assays. A luciferase reporter gene was placed under the control of a minimal tk promoter downstream from tetracycline operator DNA sequences. This reporter plasmid was cotransfected with expression vectors for ScFv/TetR or (320-393)/TetR without or with expression vectors for wild-type p53, His273, Gly281 or His175 p53 mutants in H358, a p53 null lung tumor cell line (Figure 5a). Wild-type p53 repressed the tet/tk promoter, an activity known to be exerted by wild-type p53 on several promoters (Ginsberg *et al.*, 1991). This repression was somewhat relieved by the two chimeras to achieve, however, a level of gene expression close to the basal level. Coexpression of any of the chimeras with the His273 and Gly281 p53 mutant but not with the His175 mutant led to enhanced gene expression. This latter result was expected as it had been reported that the His175 transactivation domain was non functional (Fields and Jang, 1990). Identical results were obtained with the NLS containing ScFv/TetR molecules (data not shown). Reminiscent of the coimmunoprecipitation assays, ScFv/TetR was about half as efficient as (320-393)/TetR, suggesting a lower binding of this fusion molecule to p53. As these results were obtained with exogenously produced p53 proteins, we next examined the functionality of the chimeric factors in a non transformed cell line and in tumor cell lines expressing endogenous wild-type or mutant p53. The reporter gene containing vector and the ScFv/TetR or (320-393)/TetR expression vectors were cotransfected in the non transformed NIH3T3 (wt/wt) cell line and in the transformed H460 (wt/wt) and H322 (-/Leu248) cell lines. Transcriptional transactivation was mediated by ScFv/TetR and (320-393)/TetR in H322 but not in NIH3T3 or H460 cell lines (Figure 5b). As the two chimeras were correctly expressed in the three cell lines, these results suggest that the endogenous p53 mutant expressed in H322 was specifically recruited to mediate this effect.

The SV40 Large T antigen has been previously used as a fusion to the Gal4 DNA binding domain to trap exogenously expressed mutant p53 to direct specific gene expression (Da Costa *et al.*, 1996). We have

provided evidence that single chain antibodies can also be utilized as the basis of functional entities mediating tumor specific gene expression, using a similar p53-based model. Specific gene expression was not only observed with mutant p53 introduced in a p53 null cell line but also in the H322 cell line expressing an endogenous mutant p53. This new class of synthetic molecules could be referred as 'trabodies' for transcription activating antibodies. Necessary technical improvements would have to be achieved before 'trabodies' could be incorporated in gene therapy applications. Comparisons between the results obtained with ScFv/TetR and (320-393)/TetR indicate that stronger transactivating abilities could probably be achieved by utilizing a scFv derived from a monoclonal antibody with higher affinity. Indeed, pAb421 is a monoclonal antibody that poorly binds p53. In addition, the choice of alternate linkers between the scFv and TetR may provide a more functional transactivator. The incorporation of NLS turned out not to be necessary as the ScFv/TetR chimera was localized within the nucleus. Finally, the relative positioning of the tet operator sequences within the promoter could probably be optimized to achieve a higher level of transactivation. The possibility to use tetracycline or tetracycline analogs to switch gene expression on and off (Kistner *et al.*, 1996) could provide a clinically relevant tool.

Due to the universality of ScFvs to serve as ligands, the tumor specific gene expression system that we have developed with an anti-p53 scFv could be adapted to other molecular targets relevant of pathological situations. ScFvs may also provide a specificity advantage over naturally occurring ligands which may associate with additional, undesired cellular partners (such as SV40 large T antigen which binds Rb family members in addition to p53). Ideally these pathology-associated targets should possess a functional transactivation domain and would thus be particularly suitable for antiviral strategies since viruses often encode transcriptional transactivators. One can also envision implementing the 'trabodies' technology in targeting proteins lacking transactivating domains. A system could be developed in which the target would bridge two scFv fusion proteins. The first fusion would tether an anti-target scFv to the TetR domain while the second chimera would connect a second anti-target scFv to an activation domain such as the VP16 domain. The use of scFv libraries associated to phage display screening technologies (Persic *et al.*, 1997b) would permit the rapid development of the tools necessary to design 'trabodies'.

#### Acknowledgements

This work was supported by the BioAvenir Programme (MENESR)

#### References

- Arai N, Nomura D, Yokota K, Wolf D, Brill E, Shohat O and Rotter V. (1986). *Mol. Cell. Biol.*, **6**, 3232-3239.
- Ayoubi TA and Van De Ven WJ. (1996). *FASEB J.*, **10**, 453-460.

- Bioeca S, Pierandrei-Amaldi P, Campioni N and Cattaneo A. (1994). *Biotechnology*, **12**, 396-399.
- Byk G, Scherman D and Schwartz B. (1997). Patent WO 9625508-A1.

line  
rter  
ase  
uree  
ig),  
The  
ors  
The

- Chen SY, Zani C, Khouri Y and Marasco WA. (1995). *Gene Ther.*, **2**, 116–123.
- Chen JD, Yang Q, Yang AG, Marasco WA and Chen SY. (1996). *Hum Gene Ther.*, **7**, 1515–1525.
- Cochet O, Kenigsberg M, Delumeau I, Caron de Fromentel et al. accompanying manuscript tirone–Oddos A, Multon M-C, Fridman WH, Schweighoffer F, Teillaud J-L and Tocque B. (1998). *Cancer Res.*, in press.
- Da Costa LT, Jen J, He TC, Chan TA, Kinzler KW and Vogelstein B. (1996). *Proc. Natl. Acad. Sci. USA*, **93**, 4192–4196.
- de Kruijff J and Logtenberg T. (1996). *J. Biol. Chem.*, **271**, 7630–7634.
- Fields S and Jang SK. (1990). *Science*, **249**, 1046–1049.
- Fields S and Sternglanz R. (1994). *Trends Genet.*, **10**, 286–292.
- Glockshuber R, Malia M, Pfitzinger I and Pluckthun A. (1990). *Biochemistry*, **29**, 1362–1367.
- Goldfarb DS, Garipey J, Schoolnik G and Kornberg RD. (1986). *Nature*, **322**, 641–644.
- Gossen M and Bujard H. (1992). *Proc. Natl. Acad. Sci. USA*, **89**, 5547–5551.
- Ginsberg D, Mechta F, Yaniv M and Oren M. (1991). *Proc. Natl. Acad. Sci. USA*, **88**, 9979–9983.
- Hainaut P, Soussi T, Shomer B, Hollstein M, Greenblatt M, Hovig E, Harris CC and Montesano R. (1997). *Nucleic Acids Res.*, **25**, 151–157.
- Harris CC. (1993). *Science*, **262**, 1980–1981.
- Hu S, Shively L, Raubitschek A, Sherman M, Williams LE, Wong JY, Shively JE and Wu AM. (1996). *Cancer Res.*, **56**, 3055–3061.
- Huston JS, Levinson D, Mudgett-Hunter M, Tai MS, Novotny J, Margolies MN, Ridge RJ, Brucoleri RE, Haber E and Crea R et al. (1996). *Proc. Natl. Acad. Sci. USA*, **85**, 5879–5883.
- Jannot CB, Beerli RR, Mason S, Gullick WJ and Hynes NE. (1996). *Oncogene*, **13**, 275–282.
- Kistner A, Gossen M, Zimmermann F, Jerecic J, Ullmer C, Lubbert H and Bujard H. (1996). *Proc. Natl. Acad. Sci. USA*, **93**, 10933–10938.
- Kreis TE. (1986). *EMBO J.*, **5**, 931–941.
- Luo Y, Batalao A, Zhou H and Zhu L. (1997). *Biotechniques*, **22**, 350–352.
- Mhashilkar AM, Bagley J, Chen SY, Szilvay AM, Helland DG and Marasco WA. (1995). *EMBO J.*, **14**, 1542–1551.
- Moritz D and Groner B. (1995). *Gene Ther.*, **2**, 539–546.
- Nilson BH, Morling FJ, Cosset FL and Russell SJ. (1996). *Gene Ther.*, **3**, 280–286.
- Pack P and Pluckthun A. (1992). *Biochemistry*, **31**, 1579–1584.
- Persic L, Righi M, Roberts A, Hoogenboom HR, Cattaneo A and Bradbury A. (1997a). *Gene*, **187**, 1–8.
- Persic L, Roberts A, Wilton J, Cattaneo A, Bradbury A and Hoogenboom HR. (1997b). *Gene*, **187**, 9–18.
- Pilkington GR, Duan L, Zhu M, Keil W and Pomerantz RJ. (1996). *Mol. Immunol.*, **33**, 439–450.
- Reihnsaus E, Kohler M, Kraiss S, Oren M and Montenarh M. (1990). *Oncogene*, **5**, 137–145.
- Richardson JH and Marasco WA. (1995). *Trends Biotechnol.*, **13**, 306–310.
- Richardson JH, Sodroski JG, Waldmann TA and Marasco WA. (1995). *Proc. Natl. Acad. Sci. USA*, **92**, 3137–3141.
- Shaulian E, Zauberman A, Ginsberg D and Oren M. (1992). *Mol. Cell. Biol.*, **12**, 5581–5592.
- Schmidt M, Hynes NE, Groner B and Wels W. (1996). *Int. J. Cancer*, **65**, 538–546.
- Wels W, Beerli R, Hellmann P, Schmidt M, Marte BM, Kornilova ES, Hekele A, Mendelsohn J, Groner B and Hynes NE. (1995). *Int. J. Cancer*, **60**, 137–144.

The  
Engl  
will  
poly  
encc  
tran

We  
stat  
tran  
tran  
mee  
Tur

The  
wil  
acc

Fo

ht

or

A  
M  
IC  
In  
4  
L  
U  
T  
F  
E



# Antibody fragments from a 'single pot' phage display library as immunochemical reagents

Ahuva Nissim<sup>1</sup>, Hennie R. Hoogenboom<sup>2</sup>,  
Ian M. Tomlinson<sup>1,3</sup>, Greg Flynn<sup>4</sup>,  
Carol Midgley<sup>5</sup>, David Lane<sup>5</sup> and  
Greg Winter<sup>1,3</sup>

<sup>1</sup>MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, <sup>2</sup>Cambridge Antibody Technology, The Science Park, Melbourn, Cambridgeshire SG8 6EF, <sup>3</sup>MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK, <sup>4</sup>Institute of Molecular Biology, University of Oregon, Eugene, OR 97403, USA and <sup>5</sup>Department of Biochemistry, University of Dundee, Dundee DD1 4HN, UK

Communicated by G. Winter

The display of repertoires of antibody fragments on the surface of filamentous bacteriophage offers a new way of making antibodies with predefined binding specificities. Here we explored the use of this technology to make immunochemical reagents to a range of antigens by selection from a repertoire of  $>10^8$  clones made *in vitro* from human V gene segments. From the same 'single pot' repertoire, phage were isolated with binding activities to each of 18 antigens, including the intracellular proteins p53, elongation factor EF-1 $\alpha$ , immunoglobulin binding protein, rhombotin-2 oncogene protein and sex determining region Y protein. Both phage and scFv fragments secreted from infected bacteria were used as monoclonal and polyclonal reagents in Western blots. Furthermore the monoclonal reagents were used for epitope mapping (a new epitope of p53 was identified) and for staining of cells. This shows that antibody reagents for research can be readily derived from 'single pot' phage display libraries.

**Key words:** immunochemical reagents/immunoglobulins/phage/scFv

## Introduction

Animal immunization has provided a wealth of valuable antisera and monoclonal antibodies as research reagents. However, the display of small peptides (Smith, 1985) and folded proteins (Bass *et al.*, 1990; McCafferty *et al.*, 1990) on filamentous phage, offers another source of such reagents. Thus antibody fragments have been made in bacteria by selection from repertoires of variable domains displayed on the surface of filamentous bacteriophage (for review see Hoogenboom *et al.*, 1992; Marks *et al.*, 1992a). Heavy and light chain variable domains are displayed by fusion to the viral coat protein, allowing phage with antigen binding activities (and encoding the antibody fragments) to be selected by panning on antigen. The selected phage can be grown after each round of panning and selected again, and rare phage ( $<1/10^7$ ) isolated over several rounds of panning (McCafferty *et al.*, 1990). By interposing an amber mutation between the antibody fragment and coat protein,

the fragments can also be secreted from infected bacteria as soluble fragments (Hoogenboom *et al.*, 1991). As in the immune system, selected antibodies from the primary library can be mutated, and those with improved affinities isolated (Hawkins *et al.*, 1992; Marks *et al.*, 1992b).

The repertoires of fragments, displayed on phage as single chain Fv fragments (McCafferty *et al.*, 1990) or Fab fragments (Hoogenboom *et al.*, 1991), are encoded by rearranged V genes. Diverse repertoires of heavy ( $V_H$ ) and light ( $V_L$ ) chain V genes can be derived from populations of lymphocytes (Sastry *et al.*, 1989; Ward *et al.*, 1989) using the polymerase chain reaction (PCR) (Saiki *et al.*, 1985; Orlandi *et al.*, 1989), and paired at random to encode diverse repertoires of fragments (Huse *et al.*, 1989). Immunization enriches the mRNA for  $V_H$  and  $V_L$  genes encoding antigen binding activities (Burton, 1991; Winter and Milstein, 1991), but requires a different library for each antigen.

By contrast, the use of larger and more diverse repertoires, either from V genes rearranged *in vivo* (Marks *et al.*, 1991a) or *in vitro* (Hoogenboom and Winter, 1992), can allow the isolation of antibodies of different binding specificities, without immunization, from the same library, as proposed by Milstein (1990). Such libraries have been used to produce antibodies against haptens, and foreign and self antigens (Marks *et al.*, 1991a; Hoogenboom and Winter, 1992; Griffiths *et al.*, 1993). Here we have explored the use of the same 'single pot' library to isolate antibodies with specificities that have proved difficult by hybridoma technology, for example against highly conserved intracellular proteins, and to use the phage and the encoded scFv fragments as immunochemical reagents.

## Results

### Selection of clones of different specificities

We built diverse repertoires of rearranged  $V_H$  genes *in vitro* from a bank of 50 cloned human  $V_H$  gene segments (Tomlinson *et al.*, 1992) and random nucleotide sequence encoding CDR3 lengths of 4–12 residues. The library was subjected to four or five rounds of selection against 18 antigens, including haptens, foreign and self-antigens, as well as intracellular antigens (Figure 1). Phage or secreted scFv fragments were screened for binding to the selecting antigen by ELISA, as a 'polyclonal' population and also as isolated clones. In all cases, phage with binding activities were detected to the selecting antigen. For some clones (see legend to Table I), binding activities were detected as phage but not as scFv fragments using supernatants from infected bacteria.

To obtain a diverse set of fragments for each antigen, clones with binding activities were screened for  $V_H$  family by hybridization, and for CDR3 length by PCR (see Materials and methods). Different clones were selected for sequencing. A range of CDR3 loop sizes were detected for several antigens, for example, loops of four, five, nine and

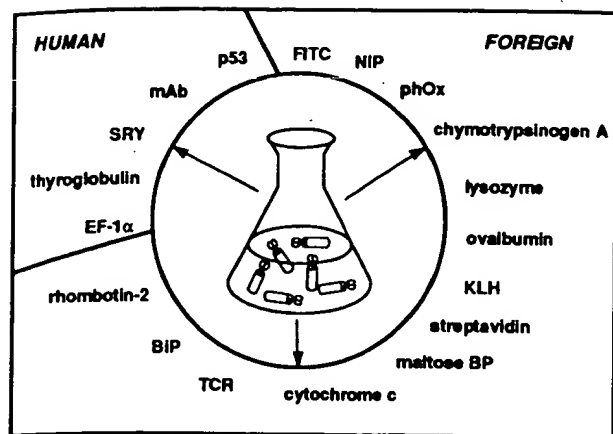


Fig. 1. Specificities from a 'single pot' human synthetic library. FITC, fluorescein isothiocyanate; NIP, 4-hydroxy-5-iodo-3-nitrophenylacetyl; phOx, 2-phenyl-5-oxazolone; KLH, haemocyanin from keyhole limpet; maltose BP, maltose binding protein; TCR, soluble chimeric murine T cell receptor; BIP, recombinant rat immunoglobulin binding protein; EF-1 $\alpha$ , human elongation factor-1 $\alpha$ ; SRY, human sex-determining region Y protein; mAb, anti-erythrocyte rhesus D antibody Oak-3; p53, human tumour suppressor protein p53.

ten residues for the hapten NIP. Over all the antigens, V<sub>H</sub> segments were found from each of the V<sub>H</sub> families except the small V<sub>H</sub>2 family, as were all the CDR3 loop lengths represented in the library (Table I). Eight residue CDR3 loops were frequent. As *in vivo* (Zouali and Theze, 1991), segments of the V<sub>H</sub>3 family (35/54) were well represented.

### Western blots

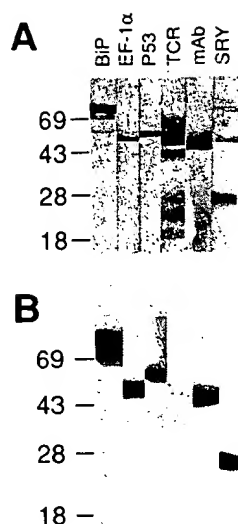
Phage and scFv fragments were used as 'polyclonal' and monoclonal reagents for Western blots. 'Polyclonal' phage, prepared by PEG precipitation, were used in Western blotting (Towbin *et al.*, 1979) to detect a panel of purified antigens on nitrocellulose after PAGE (Figure 2A); anti-EF-1 $\alpha$  phage were also used to detect EF-1 $\alpha$  in COS cell lysates (not shown). Similarly 'polyclonal' scFv fragments, concentrated 10-fold by dialysis against PEG from the bacterial supernatants, were used to detect the panel of antigens (Figure 2B); and to detect p53 in lysates of the breast cancer (T47D) cells with high levels of mutant human p53 protein (Bartek *et al.*, 1990). p53 was not detected in lysates of a human osteosarcoma cell line (SAOS-2) with a genetic deletion of both p53 genes (Masuda *et al.*, 1987) (Figure 3).

Monoclonal scFv fragments derived from segments of the

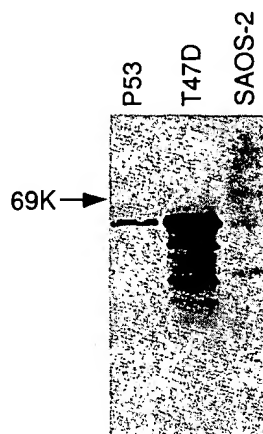
Table I. Deduced V<sub>H</sub>-CDR3 sequences and germline origin of selected antigen-specific synthetic antibodies isolated from a single pot human synthetic library

Self	CDR3 sequences	V <sub>H</sub> segment	Foreign	CDR3 sequences	V <sub>H</sub> segment
anti-RhD mAb (Oak-3)	RRPTGHHW	DP-53	rhombotin-2	QVYQA	DP-46
thyroglobulin	RHNGNWD	DP-53		YTRKRFRPPER	DP-47
	VARYNMYIPP	DP-49	recombinant	TRHARFDY	DP-14
	SKGAWFVRPP	DP-49	rat BiP	TWPTK (#17)	DP-32
	MKSSARPV	DP-66		GYTPFNY (#2)	DP-33
EF-1 $\alpha$	VYPFRBTN	DP-51		GKRYFTK	DP-42
	INGKKFDY	DP-73		TRRSRFDY	DP-67
p53	NQNV	DP-45		GRHSRFDY	DP-67
	NQHV	DP-45	mouse TCR	GKGPSYTAILSF	DP-10
	FTRKRD (#30)	DP-53		SYHHLFDY	DP-46
SRY	QNLHNNQLV	DP-2		GFAYIFDY	DP-74
	RTPAVLSQB RNV	DP-42	maltose BP	NWRNSFPQ	DP-14
	MAIQT	DP-47		SSNPWK	DP-14
	SWRGLMM	DP-70		ELMYFV	DP-48
Haptens	CDR3 sequences	V <sub>H</sub> segment		TPIHRRRQFNTG	DP-53
NIP	VMSSADGHR	DP-38		YRTAHL	DP-67
	RGMN	DP-42	turkey egg	SYNEIVPI	DP-3
	KGGFD	DP-42	lysozyme	NYQLBVPQ	DP-3
	GGTR	DP-42	cytochrome c	RIGTPFDY	DP-3
	SGRD	DP-42	KLH	LRHGF	DP-45
	RRGPAGAYYP	DP-47	ovalbumin	RRHRAFDY	DP-47
phOx	TRAYRFDY	DP-47	chymotrypsinogen A	GWNASD	DP-7
	LRNFSFDY	DP-47		KKBI	DP-58
	RNAWGLIAARRT	DP-53		SKBI	DP-58
FITC	SSKWSMRN	DP-7	streptavidin	DWRMIEG	DP-49
	ALQGPAYST	DP-35		QWEGIRS	DP-69
	EHRTSIPT	DP-42			
	LRARPV	DP-67			

The encoded sequences of V<sub>H</sub>-CDR3, the third complementarity determining region of the antibody heavy chain are given. Nomenclature of the heavy chain germline segments is as in Tomlinson *et al.* (1992). The specificities were detected as phage and also in bacterial supernatants as soluble scFv fragments, except for anti-thyroglobulin, EF-1 $\alpha$ , SRY, turkey egg lysozyme, ovalbumin, chymotrypsinogen A and streptavidin, which were initially detected only as phage antibodies. B represents translation of amber codon to glutamine in *E. coli* TG-1 *supE* strain. Abbreviations as in Figure 1.



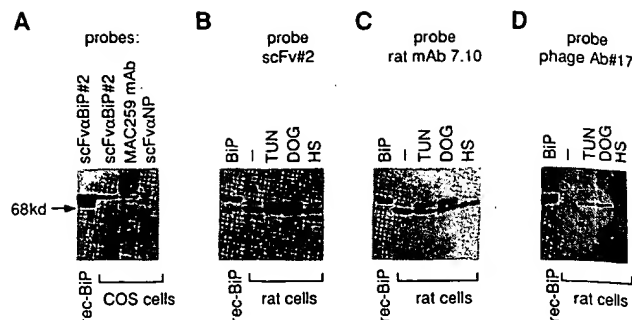
**Fig. 2.** Western blotting with polyclonal phage and fragments antibodies. 2  $\mu$ g of purified antigens were electrophoresed under reducing conditions on 10% acrylamide gels, electroblotted to nitrocellulose and hybridized with polyclonal phage antibodies (A) or polyclonal scFvs (B). The expected molecular weights of BiP, EF-1 $\alpha$ , p53, TCR, mAb and SRY are respectively 78, 53, 53, 43, 50 ( $\gamma$ 3 heavy chain) and 26 kDa.



**Fig 3.** Detection of p53 in cell lysates by 'polyclonal' scFv fragments. Human p53 (2  $\mu$ g) purified from SF9 insect cells infected with a recombinant baculovirus encoding wild type human p53 (Luckow and Summers, 1989; C.A.Midgley, unpublished), cell lysates ( $10^5$  cells) of T47D human breast cancer cell line (overexpresses p53) and SAOS-2 human osteosarcoma cell line (in which both p53 genes are deleted).

human V<sub>H</sub>3 family (and therefore binding to protein A) (Sasso *et al.*, 1991) were chosen for use as reagents, as they could be purified by binding to protein A-Sepharose (Hoogenboom and Winter, 1992), and as reagents readily detected with horseradish peroxidase (HRP)-protein A. (The fragments of other families, or indeed the V<sub>H</sub>3 family, could be detected by their C-terminal peptide tag using the mouse monoclonal antibody 9E10 followed by HRP-goat anti-mouse IgG.) Analysis of the scFv fragments by gel filtration, for example those described here against p53 and BiP, indicated that the fragments were partly aggregated, as shown previously with scFv fragments derived from phage display repertoires (Griffiths *et al.*, 1993) or from monoclonal antibodies (Holliger *et al.*, 1993).

In lysates of COS cells, a purified monoclonal scFv



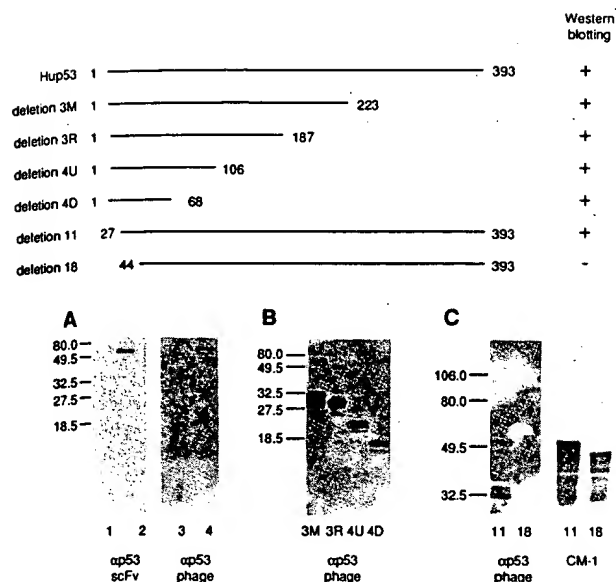
**Fig. 4.** Detection of hsp70 proteins by monoclonal anti-BiP scFv fragments and phage. (A) Detection of recombinant rat BiP and BiP in COS cell lysates with anti-BiP scFv #2, with controls of MAC256 monoclonal antibody (recognizing a KDEL motif shared by luminal ER proteins) and a scFv (directed against the hapten NP). (B-D) Specificity of anti-BiP scF fragments (B and C) or phage (D). Rat cells (RAT-1) were incubated for 19 h without drugs (-), or with 0.5  $\mu$ g/ml tunicamycin (TUN), or with 10 mM 2-dioxy-D-glucose (DOG), or were heat shocked for 1 h at 42°C (HS). scFv #2 and rat mAb 7.10 recognize the hsp70 family. However, phage #17 reacts only with BiP, induced by TUN or DOG treatment but not by HS.

fragment (scFv $\alpha$ BiP #2) against recombinant rat BiP (immunoglobulin binding protein, and identical to glucose regulated protein grp78) (Munro and Pelham, 1986) detected a band of  $\sim$ 70 kDa, corresponding to 'cognate' cytosolic stress-70 proteins (hsc70) (Figure 4A). Likewise in lysates of rat fibroblast (RAT-1) cells (Figure 4B) the reagent mainly detected a single band of  $\sim$ 70 kDa, as does the control 7.10 mAb (Palter *et al.*, 1986) which is known to bind to several members of the hsp70 protein family including 'cognate' hsc70, heat inducible hsp70 and BiP (Figure 4C). The scFv fragments appear to be as sensitive as monoclonal antibodies as reagents. A solution of 10  $\mu$ g/ml of scFv #2 reagent readily detected 15 ng recombinant BiP spotted onto nitrocellulose, resulting in strong staining by ECL.

BiP is present at low levels in fibroblasts; it is not heat inducible but the rate of its synthesis is increased when cells are starved for glucose or when induced by glycosylation inhibitors such as tunicamycin or 2-dioxy-D-glucose (Pouyssegur *et al.*, 1977; Olden *et al.*, 1979). When RAT-1 cells were treated, both the scFv reagent and the 7.10 mAb detected the appearance of a second band of  $\sim$ 80 kDa, presumably BiP (Figure 4B and C). Thus the scFv fragments appear to have a similar specificity to mAb 7.10. However, we also isolated more specific fragments that recognized only BiP, and not hsc70 (or the heat inducible hsp70) (Figure 4D), as illustrated here with a monoclonal phage reagent #17.

#### Epitope mapping

The epitope on p53 was mapped using monoclonal phage or scFv as a reagent (#30, CDR3: FTRKRD) Both phage and scFv fragment detected recombinant human p53 expressed in bacteria (Figure 5A), and also a series of p53 proteins deleted at the C-terminus (Figure 5B). This localized the epitope to the N terminus of p53. Mapping of two p53 proteins deleted at the N-terminus (Figure 5C) indicates that the epitope lies between residues 27 and 44 since a p53 fragment encoding amino acids 44-393 was not detected. The results were confirmed with the soluble scFv fragment reagent (not shown). The localization of epitope is consistent with the observation that the binding of the scFv fragment is not blocked by the DO-1 antibody (not shown), which



**Fig. 5.** Mapping the epitope in p53 recognized by an scFv fragment. The figure shows the portions of the p53 fragments expressed in bacteria and their reactivity with an anti-human p53 scFv fragment or corresponding phage on Western blots. (A) Western blot of lysate from induced *E. coli* containing pT7-7 vector only (lanes 1 and 3) or pT7-7Hup53 which direct the expression of full length human p53 (lanes 2 and 4). (B and C) Western blots of lysate from induced *E. coli* containing 3' (B) or 5' (C) truncated pT7-7Hup53. Anti-p53 phage antibodies detected all of the deleted proteins except deletion 18. CM-1 rabbit polyclonal anti-human p53 antibodies were used as positive control in (C).

recognizes an immunodominant site within the first 27 amino acids of the protein (D.Lane, unpublished data).

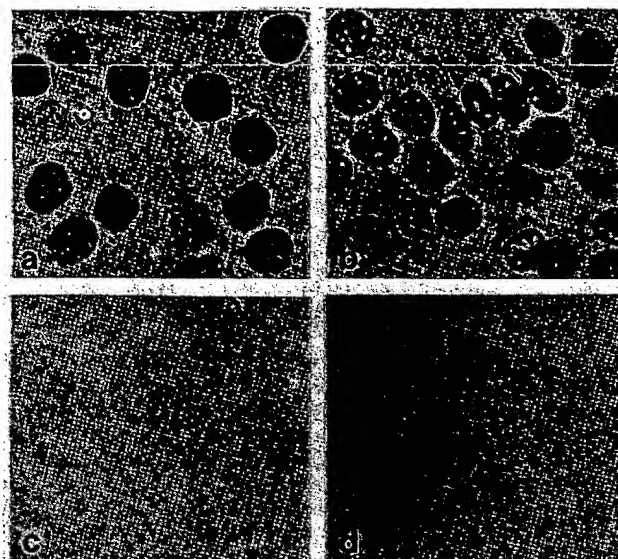
### Immunocytochemistry

Monoclonal anti-p53 scFv fragments (#30) were used to stain the breast cancer cell line T47D. Clear nuclear staining of the T47D cells was seen when the scFv was used at a concentration of 10  $\mu$ g/ml. At this concentration only a very low level of non-specific staining was seen when the same reagents were applied to the human SAOS-2 cells (Figure 6) or mouse C6 cells (and indicating that the scFv fragment does not bind mouse p53). We failed to find conditions for specific staining of the nucleus with the anti-p53 phage; presumably the phage particle is too large to penetrate.

### Discussion

We have shown that phage with a range of binding specificities, can be isolated from a 'single pot' phage antibody library (Figure 1) within a few days and without animal immunization. We could isolate binding specificities to haptens, foreign and self-antigens, including secreted proteins (lysozyme and ovalbumin), cell surface proteins (T cell receptor), intracellular proteins from the cytoplasm (thyroglobulin, EF-1 $\alpha$ ), proteins from the lumen of the endoplasmic reticulum (BiP) and proteins from the nucleus (p53, SRY and rhombotin-2).

Phage and scFv fragments from the single pot library could be used without further affinity maturation as immunological reagents for Western blotting, epitope mapping and cell staining. We also used phage and scFv fragments in monoclonal and polyclonal formats. Polyclonal reagents are



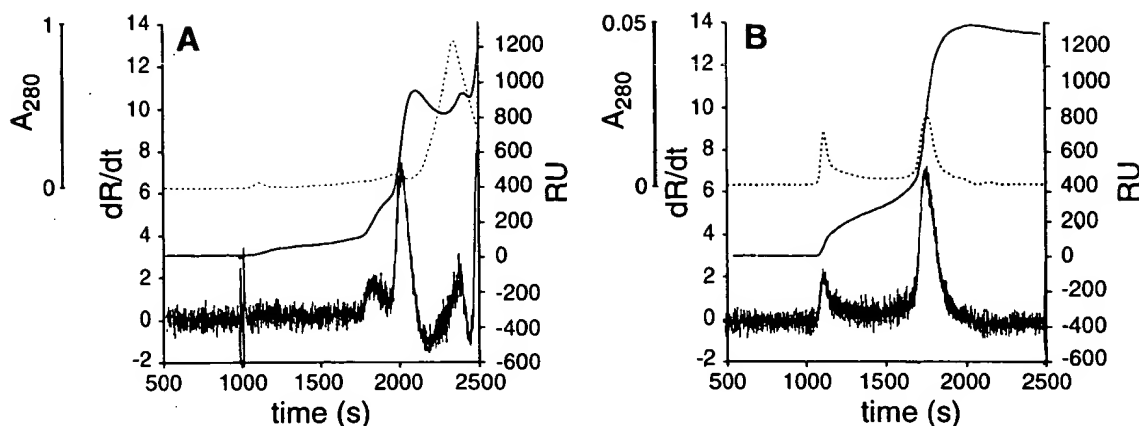
**Fig. 6.** Immunocytochemistry using monoclonal scFv. Staining of T47D (a and b) and SAOS-2 cells (c and d). (a) and (c) show staining with monoclonal anti-p53 scFv fragment, while (b) and (d) show staining by mouse monoclonal anti-p53 antibody (DO-1).

simpler to prepare, as the presence of binding phage can be readily detected by ELISA, and the phage population (or soluble scFv fragments) can then be used directly, or after affinity purification. In particular, scFv fragments derived from segments of the human V<sub>H</sub>3 family (and therefore binding to protein A) could be readily purified with protein A-Sepharose, and as reagents readily detected with protein A-HRP conjugates.

Although for each of the antigens we could isolate phage clones with binding activities, we were sometimes unable to detect binding of the encoded soluble scFv fragments using bacterial supernatants. This may reflect the amplified detection of the phage by virtue of the 3000 subunits of the phage 'tail': if so, a more sensitive assay should be used for the soluble fragments. It might also reflect the greater binding avidities afforded by multivalent display on phage, and the moderate binding affinities of the monomeric scFv fragments from primary phage repertoires of  $10^7$ – $10^8$  clones (Marks *et al.*, 1991a; Hoogenboom and Winter, 1992; Griffiths *et al.*, 1993).

We found that the scFv fragments in supernatants could be more readily detected by concentrating the supernatant, or by 'multimerization' of the fragments during purification. Although scFv fragments can associate to form dimers in bacterial supernatants (Griffiths *et al.*, 1993; Holliger *et al.*, 1993), and the dimers have greater binding avidities to solid phase antigen (Griffiths *et al.*, 1993), purification can also drive the formation of multimers (Figure 7). Presumably multimerization is promoted by dissociation of V<sub>H</sub> and V<sub>L</sub> domains of the same chain, followed by pairing with another chain, especially during acid elution and neutralization in concentrated solutions. Indeed the purified scFv fragments used to detect p53 and BiP in Western blotting, epitope mapping and cell staining were partly aggregated (Figure 7).

Aggregation of 'moderate affinity' scFv fragments is probably important for their use as immunological reagents as it enhances the avidity of binding and slows the rate of dissociation during washing. Clearly antigen should be provided in multimeric form, for example immobilized on



**Fig. 7.** Combined FPLC/BIAcore analysis of anti-BiP #2 scFv. Bacterial culture supernatant (A) and protein A affinity purified anti-BiP scFv #2 (B) were fractionated on a Superdex 200 column, with the eluent monitored by both UV 280 nm absorbance (upper, dotted line) and on-line BIAcore with immobilized 9E10 on the sensor chip (middle curve, light solid line). FPLC standards: of hen egg lysozyme (2455 s;  $M_r$  14.3 kDa), hen ovalbumin (1900 s; 45 kDa), BSA monomer (1780 s; 68 kDa) and BSA dimer (1590 s; 136 kDa), were used to calibrate the FPLC column. The derivatized sensorgram (dR/dt, lower, heavy solid line) illustrates the rate of changes in mass of protein bound to the sensor chip as a function of time. Note that the various y-axes have been scaled with zero at different levels for clarity. In (A), the main peak of binding near 2020 s corresponds to monomeric scFv, with a small peak of more aggregated material at 1830 s. The disturbance near 1000 s is an artifact caused by pump filling; the exclusion volume corresponds to 1100 s on the traces shown. In (B) there is substantial material at or near the exclusion volume (1120 s); the main peak (1750 s) most closely corresponds to a mixture of trimer and tetramer, with only minor amounts of dimer and monomer.

nitrocellulose as in Western blots, or in fixed cells, and at high density to allow crosslinking with multimeric antibody. Furthermore the use of high density antigen should also facilitate the rebinding of multimeric and even monomeric fragments, slowing the net rate of dissociation from the solid phase. It would therefore be desirable to drive the self-aggregation of scFv fragments, for example by use of dimerization peptides (Pack and Pluckthun, 1992) or by shortening the flexible linker (Holliger *et al.*, 1993). However, scFv fragments are also aggregated by binding to protein A or to the bivalent mouse monoclonal antibody 9E10.

Not only have the single pot libraries provided a range of immunochemical reagents, but monoclonal specificities that are difficult to make by hybridoma technology, for example against the elongation factor 1 $\alpha$  (EF-1 $\alpha$ ) (Merrick *et al.*, 1993) and immunoglobulin heavy chain binding protein (BiP). BiP is located in the lumen of the endoplasmic reticulum (see Gething and Sambrook, 1992), and is a member of a family of hsp70-related proteins that includes cytosolic 'cognate' hsc70 (p73) and heat inducible hsp70 (p72). BiP binds to partially folded or unassembled proteins, blocking their transport through the endoplasmic reticulum, and is highly conserved between species. Only one monoclonal antibody specific for BiP (Bole *et al.*, 1986), has been reported, and other less specific monoclonal antibodies have been used as reagents. For example, rat monoclonal antibody (7.10) raised against *Drosophila* hsp70 also binds to BiP (and to hsp70s and hsp-70-related proteins from a wide range of species) (Palter *et al.*, 1986), and antibodies against the C-terminal (KDEL) tetrapeptide of BiP, also bind to other KDEL proteins (including grp94 and protein disulfide isomerase) (Pelham, 1989). Presumably antibodies against BiP are retained in the lumen of the endoplasmic reticulum of B-cells and are difficult to display or secrete (Bole *et al.*, 1986). However, from the single pot library, we could readily isolate an anti-BiP reagent that reacts specifically with rat BiP in rat cell lysates, and also a more cross-reactive reagent that recognizes hsc70 (and with similar specificity to rat 7.10).

There is also a hint that the phage may recognize different epitopes, or at least those with a different bias, from monoclonal antibodies. For example, mouse antibodies to human p53 bind to two main immunodominant regions of the protein, at the N-terminal region and at the C-terminal region (Schlichtholz *et al.*, 1992). The immunodominant region lies between amino acids 1 and 25 at the N terminus or amino acids 370 and 381 at the C terminus (D.Lane, unpublished data); the epitope recognized by the anti-p53 scFv fragment appears to lie between residues 27 and 44. This portion of sequence differs significantly between mouse and human p53, and indeed as predicted the scFv reagent does not recognize mouse p53 in cell staining (or indeed by ELISA on purified mouse p53—not shown). However, it remains to be seen whether in general the phage libraries lead to a different spectrum of epitopes from natural immune systems. If so, such reagents could prove invaluable for mapping the functions of proteins.

In conclusion, single pot libraries are capable of providing immunochemical reagents of high specificity, and in future higher affinity fragments may emerge from larger libraries (Perelson and Oster, 1979; Waterhouse *et al.*, 1993), or by affinity maturation of selected antibodies by chain shuffling (Marks *et al.*, 1992b). The use of these libraries appears to open new possibilities for immunochemistry.

## Materials and methods

### Library construction

The human synthetic libraries (HSL) were constructed as in Hoogenboom and Winter (1992) using PCR primers designed to introduce  $V_H$ -CDR3 of random sequence varying in length from 4 to 12 residues. All 49 germline  $V_H$  segments amplified in Hoogenboom and Winter (1992) were used except for DP-44 (as this produces an identical product to DP-45; see Tomlinson *et al.*, 1992), and two additional  $V_H$ 2 segments (DP-26 and DP-28) were incorporated. Note that several of these segments are not seen as rearranged genes, and lie outside the main  $V_H$  locus (unpublished data). DNA template encoding each of the 50 germline  $V_H$  segments was individually amplified using the  $V_H$  family based primers (Marks *et al.*, 1991a) VHBCKSfi and HSLP4-HSLP12 (Table II) in a volume of 50  $\mu$ l with 250  $\mu$ M dNTPs, 10 mM KCl, 10 mM  $(NH_4)_2SO_4$ , 20 mM Tris-HCl (pH 8.8), 2 mM  $MgCl_2$ , 100  $\mu$ g/ml BSA and 1  $\mu$ l (1 unit) of Taq DNA

Table II. Oligonucleotide primers used to create the synthetic library

HSLP	5'-GAC CAG GGT ACC TTG GCC CCA [(A/C)NN] <sub>n</sub> TCT TGC ACA GTA ATA CAC GGC CGT GTC
JHSAL	5'-GCC TGA ACC GCC TCC ACC <u>AGT CCA</u> CAC GGT GAC CAG GGT ACC TTG GCC CCA
CDRFOR	5'-CAG GGT ACC TTG GCC CCA
CDRBACK	5'-GTG TAT TAC TGT GCA AGA

Each germline V<sub>H</sub> segment (Tomlinson *et al.*, 1992) was amplified using V<sub>H</sub> family based primers (Marks *et al.*, 1991a) VHBACSFs and HSLP. The HSLP primers were designed to introduce a J segment and a random D segment of 4–12 residues (A/C, N, N)<sub>n</sub> where *n* = 4–12. The 3' portion of the oligonucleotide was designed to anneal with FR3 of the germline V<sub>H</sub> gene segments. The JHSAL primers were designed to introduce a *SalI* restriction site (underlined) to the 3' end of each amplified germline V<sub>H</sub> segment for cloning, and the CDRFOR and CDRBACK primers to amplify CDR3. Regions of primers based in the J segment are marked in bold, and in italics for regions based in FR3

polymerase. Template was provided as 10<sup>6</sup> bacteria of a stock infected with recombinant M13 encoding each V<sub>H</sub> segment. 25 cycles (94°C for 1 min, 55°C for 1 min and 72°C for 1.5 min) were used, with limiting VHBACSFs and HSLP primers (0.25 pmol/μl) to exhaust the primers.

In a second PCR step, a *SalI* restriction site was introduced at the 3' end of the J<sub>H</sub> segment. 30 pmol of the same VHBACSFs oligonucleotide and 30 pmol of JHSAL (Table II) were added, and the PCR continued for additional 15 cycles. After checking that a band of the appropriate size was observed on agarose gel electrophoresis for each of the 450 samples (9 × 50), the PCR products of each of the amplifications encoding the nine different CDR3 loop lengths were pooled, cut with *NcoI* and *SalI*, and cloned into *NcoI*–*XhoI*-cut pHEN1-VX3 (Hoogenboom and Winter, 1992) to provide nine phagemid libraries, each of at least 10<sup>7</sup> different clones.

Each library was rescued separately with helper phage VCS-M13 (Stratagene), then pooled with each other, and with two earlier libraries (Hoogenboom and Winter, 1992), each of at least 10<sup>7</sup> different clones and encoding loops of five or eight residues (the latter with five random and C-terminal Phe-Asp-Tyr), to create a single pot library of > 10<sup>8</sup> clones.

#### Selection of phage library

Phage were panned for binding using immunotubes (Nunc; Maxisorp) coated with each antigen overnight at room temperature (Marks *et al.*, 1991; Griffiths *et al.*, 1993). The library was subjected to four or five rounds of selection on the various antigens.

The following antigens were coated at 100 μg/ml: human mAb (γ3, κ) anti-erythrocyte rhesus (D) monoclonal antibody (Oak-3, from Barbara D. Gorick; Bye *et al.*, 1992); human thyroglobulin (Hu-Thy; Scipac); 2-phenyl-5-oxazolone (phOx)-BSA; 4-hydroxy-5-iodo-3-nitrophenylacetyl (NIP)-BSA; turkey egg-white lysozyme (TEL; Sigma); horse heart cytochrome *c* (Sigma); keyhole limpet haemocyanin (KLH; Sigma); chicken egg ovalbumin (Ovalbumin; Sigma); α-chymotrypsinogen A (type II from bovine pancreas; Sigma); bovine serum albumin–L-fluorescein isothiocyanate (FITC-BSA; Sigma) and streptavidin from *Streptomyces avidinii* (Sigma). Coating was in 50 mM NaHCO<sub>3</sub> pH 9.6 (Oak-3, TEL, KLH, ovalbumin and chymotrypsinogen A), or PBS (human thyroglobulin, NIP, phOx, cytochrome *c*, FITC-BSA and streptavidin).

The following antigens were coated at 20 μg/ml: recombinant rat BiP (see below); human elongation factor 1α (EF-1α, from P. Kristensen; Merrick *et al.*, 1993); human p53 isolated from SF9 insect cells infected with a recombinant baculovirus encoding wild type human p53 (Luckow and Summers, 1989; C.A. Midgley, T. Hupp and D. Lane, unpublished); soluble chimeric murine T cell receptor (TCR, from K. Karjalainen; Weber *et al.*, 1992); protein encoded by the human testis determining gene, SRY (sex-determining region Y) from V.R. Harley (Harley *et al.*, 1992); fusion of rhombotin-2 to maltose binding protein (maltose BP) and recombinant mouse rhombotin-2 from T. Rabbitts (Foroni *et al.*, 1992). Coating was in PBS (BiP, TCR) or 50 mM NaHCO<sub>3</sub> pH 9.6 (p53, EF-1α, SRY, maltose BP and rhombotin-2).

The rat BiP was engineered with six N-terminal histidine residues and a factor X cleavage site preceding the mature BiP polypeptide (His-BiP). Oligonucleotide primers were used to amplify the coding region of BiP from the plasmid R76 (from H. Pelham). The amplified product was inserted into the *Bam*HI–*Hind*III restriction sites of pQE40 vector (Qiagen) encoding the His6 tail, then transformed into *Escherichia coli* strain XL-1 Blue (Stratagene). Expression and purification of His6-tagged protein over Ni-NTA resin were performed by protocols provided by the manufacturer (Qiagen). After eluting from the Ni-NTN resin with 250 mM imidazole, 200 mM NaCl, 50 mM HEPES, pH 7.0, the His-BiP was further purified by ATP-agarose affinity chromatography (Flynn *et al.*, 1989). His-BiP was > 95% pure.

#### Screening and sequencing of clones

As described (Marks *et al.*, 1991; Hoogenboom and Winter, 1992; Griffiths *et al.*, 1993), phage were rescued from single ampicillin-resistant colonies

of infected (suppressor) *E. coli* TG-1 using the helper phage VCS-M13 (Stratagene); soluble scFv fragments were induced from single colonies of infected (non-suppressor) *E. coli* HB2151 (Hoogenboom *et al.*, 1991) by IPTG. Bacterial supernatants containing phage or scFv fragments were screened for binding to antigen by ELISA. The binding specificity was checked by ELISA using plates coated with one or more other antigens: phage isolated by selection on 20 μg/ml antigens were screened against all the other antigens of this set. For the fusion proteins chimeric TCR–murine C<sub>κ</sub> and rhombotin-2-maltose BP, the specificity of the selected phage antibodies was further examined by ELISA using plates coated with mouse IgM, κ antibody and maltose BP, respectively.

Phage with binding activities were screened for CDR3 length by PCR and for V<sub>H</sub> family by hybridization. Individual phagemid colonies were amplified using γ-<sup>32</sup>P-labelled CDR-BACK and CDR-FOR primers (Table II). The size of the amplified CDR3 was followed by gel electrophoresis using 7.6 M urea–8% polyacrylamide gels. Template from the entire phage library was used to produce a ladder of CDR3 lengths. Colonies were probed as in Tomlinson *et al.* (1992) for V<sub>H</sub> family using the family-specific oligonucleotide probes (Marks *et al.*, 1991b). Different clones, as shown by different CDR lengths in combination with V<sub>H</sub> segments of different families were sequenced by the dideoxy method (Sanger *et al.*, 1977) using DyeDeoxy chain termination (Applied Biosystems Inc.) and an Applied Biosystems 373A DNA sequencer. The sequences were analysed using SeqEd (Applied Biosystems Inc.) and MacVector 3.5 (IBI Kodak, New Haven, CT).

#### Preparation of monoclonal and polyclonal reagents

For monoclonal scFv fragments, supernatants from 1 l cultures of infected HB2151 bacteria induced overnight with IPTG at 30°C (Griffiths *et al.*, 1993) were filtered with Sterivex-HV 0.45 μm filter unit (Millipore) and then purified on protein A–Sepharose (Pharmacia), as described in Hoogenboom and Winter (1992). Monoclonal phage was prepared by PEG precipitation of the supernatant of infected bacteria (Marks *et al.*, 1991). Polyclonal reagents were prepared from an aliquot of infected bacteria after the last round of selection. However, for the polyclonal scFv fragments, the supernatant was concentrated ~10-fold by dialysis against dry granular PEG-6000.

#### Western blotting

Polyclonal reagents were used to detect purified antigen on Western blots as follows. 2 μg of each purified antigen were run on 10% polyacrylamide gel and then electroblotted. Filters were blocked for 1 h at room temperature in 5% Marvel/PBS/0.2% Tween 20 (for scFv fragments) or 10% Marvel/PBS/0.5% Tween 20 (for phage). The scFv fragments (1:2 dilution of 10 × concentrated supernatant) or phage (10<sup>11</sup> TU/ml) were added and incubated overnight with gentle shaking at 4°C. After washing with PBS–0.2% Tween 20 (or PBS–0.5% Tween 20 for phage), binding of scFv fragments was detected with a mixed reagent, HRP–protein A (Sigma P8651) mixed with the mouse monoclonal antibody 9E10, and followed by HRP–goat anti-mouse Ig (Sigma). Phages were detected with sheep anti-M13 1:1000 (provided by Cambridge Antibody Technology), followed by HRP–anti-goat antibody (Sigma). Peroxidase activity was detected using an ECL kit from Amersham.

Anti-p53 polyclonal scFv fragments (~10 μg/ml) were likewise used to detect p53 in T47D breast cancer cell lysates, and polyclonal anti-EF-1α phage antibodies (10<sup>11</sup> TU/ml) to detect EF-1α in COS cell lysates. Lysates were fractionated on 10% SDS–polyacrylamide gels (Laemmli, 1970), and electrophoretically transferred onto nitrocellulose (Towbin *et al.*, 1979).

For detection of BiP in cell lysates with monoclonal reagents, cell lysates were prepared from 5 × 10<sup>6</sup> COS cells grown at 37°C in DMEM/10% FCS, or from 5 × 10<sup>6</sup> RAT-1 fibroblast cells (Munro and Pelham, 1986; Napier *et al.*, 1992). The RAT-1 cells were treated with 0.5 μg/ml tunicamycin, 10 mM 2-dioxy-D-glucose or heat shock (Munro and Pelham, 1986). The filters were treated as above, and BiP detected either with 20



$\mu\text{g/ml}$  monoclonal  $\alpha$ -BiP scFv reagent followed by  $10 \mu\text{g/ml}$  HRP-protein A; or with  $10^{11}$  TU/ml of  $\alpha$ -BiP phage (as above, except that the HRP was detected by 3,3'-diaminobenzidine in 0.02% cobalt sulfate). The rat 7.10  $\alpha$ -BiP mAb (ascites diluted 1:500; Cambridge Research Biochemicals), and the rat anti-KDEL mAb from J. Butcher (Napier et al., 1992) were detected with  $10 \mu\text{g/ml}$  anti-rat HRP.

#### Epitope mapping

Plasmid pT7-7 Hup53 directs the expression of human p53 and deletion mutants truncated at the N- or C-terminus (Vojtesek et al., 1992) in *E. coli* BL21 (DE3) cells. Total lysates from log phase cultures induced with IPTG were blotted much as above, except using 15% SDS-polyacrylamide gels. CM-1 polyclonal rabbit serum (1:300) against human p53, monoclonal  $\alpha$ -p53 scFv fragment ( $10 \mu\text{g/ml}$ ), or monoclonal  $\alpha$ -p53 phage ( $10^{11}$  TU/ml) were used to detect p53 using  $10 \mu\text{g/ml}$  HRP-protein A (Sigma P8651), or (for the phage) 1:500 rabbit anti-F1 phage anti-serum followed by HRP-swine anti-rabbit Ig (Dako). Peroxidase activity was detected using an ECL kit from Amersham.

#### Immunocytochemistry

Cell staining was performed as in Vojtesek et al. (1992). Briefly, T47D cells containing high levels of mutant human p53 protein, and SAOS-2 cells which contain a genetic deletion of both p53 genes, were passaged on plastic dishes and prefixed in cold methanol/acetone (1:1 by volume). A 2-fold dilution series (in PBS/10% fetal calf serum) of scFv fragment was spotted onto the fixed cells as  $5 \mu\text{l}$  drops and incubated at room temperature for 2 h. The cells were washed three times with PBS then incubated with HRP-conjugated protein A (Sigma,  $1 \mu\text{g/ml}$ ). Alternatively, 9E10 was used followed by HRP-goat anti-mouse IgG (Sigma). The peroxidase activity was detected with 3,3'-diaminobenzidine in 0.03% nickel sulfate.

#### Sizing of scFv fragments by combined FPLC/BIAcore analysis

Bacterial cultures of anti-BiP scFv #2 supernatants (0.5 ml of 0.2  $\mu\text{m}$ -filtered) and protein A affinity-purified fragments ( $100 \mu\text{l}$  of 1.6 mg/ml) were analysed as described by Griffiths et al. (1993). The samples were fractionated on a Superdex S200 column (Pharmacia) and were monitored both by absorbance at 280 nm and on-line by BIAcore with immobilized 9E10 on the sensor chip (Johnsson et al., 1991). The buffer was PBS containing 0.2 mM EDTA and 0.05%  $\text{NaN}_3$ . The BIAcore reading was corrected for the baseline, and also then calculated as  $\text{dR}/\text{dt}$ , the rate of change of the signal.

#### Acknowledgements

We would like to thank S. Munro, G. Walter, A.D. Griffiths for advice, T.D. Prospero for FPLC/BIAcore analysis, and many colleagues for kindly providing antigens, as acknowledged in Materials and methods. A.N. is funded by Human Frontier Science Programme Organization (HFSP), and C.M. and D.L. by the Cancer Research Campaign.

#### References

- Bartek, J., Iggo, R., Gannon, J. and Lane, D.P. (1990) *Oncogene*, **5**, 893–899.
- Bass, S., Greene, R. and Wells, J.A. (1990) *Proteins*, **8**, 309–314.
- Bole, D.G., Hendershot, L.M. and Kearney, J.F. (1986) *J. Cell Biol.*, **102**, 1558–1566.
- Burton, D.R. (1991) *Trends Biotechnol.*, **9**, 168–175.
- Bye, J.M., Carter, C., Cui, Y., Gorick, B.D., Songsivilai, S., Winter, G., Hughes-Jones, N.C. and Marks, J.D. (1992) *J. Clin. Invest.*, **90**, 2481–2490.
- Flynn, G.F., Chappell, T.G. and Rothman, J.E. (1989) *Science*, **245**, 385–390.
- Foroni, L., Boehm, T., White, A., Forster, A., Sherrington, P., Liao, X.B., Brannan, C.I., Jenkins, N.A., Copeland, N.G. and Rabbitts, T.H. (1992) *J. Mol. Biol.*, **226**, 747–761.
- Gething, M.J. and Sambrook, J. (1992) *Nature*, **355**, 33–45.
- Griffiths, A.D. et al. (1993) *EMBO J.*, **12**, 725–734.
- Harley, V.R., Jackson, D.I., Hextall, P.J., Hawkins, J.R., Berkovitz, G.D., Sockanathan, S., Lovell-Badge, B. and Goodfellow, P.N. (1992) *Science*, **255**, 453–456.
- Hawkins, R.E., Russell, S.J. and Winter, G. (1992) *J. Mol. Biol.*, **226**, 889–896.
- Holliger, P., Prospero, T. and Winter, G. (1993) *Proc. Natl Acad. Sci. USA*, **90**, 6444–6448.
- Hoogenboom, H.R. and Winter, G. (1992) *J. Mol. Biol.*, **227**, 381–388.
- Hoogenboom, H.R., Griffiths, A.D., Johnson, K.S., Chiswell, D.J., Hudson, P. and Winter, G. (1991) *Nucleic Acids Res.*, **19**, 4133–4137.
- Hoogenboom, H.R., Marks, J.D., Griffiths, A.D. and Winter, G. (1992) *Immunol. Rev.*, **130**, 41–68.
- Huse, W.D., Sastry, L., Iverson, S.A., Kang, A.S., Altling, M.M., Burton, D.R., Benkovic, S.J. and Lerner, R.A. (1989) *Science*, **246**, 1275–1281.
- Johnsson, B., Löfås, S. and Lindqvist, G. (1991) *Anal. Biochem.*, **198**, 268–277.
- Laemmli, U. (1970) *Nature*, **227**, 680–685.
- Luckow, V.A. and Summers, M.D. (1989) *Bio/Technology*, **6**, 47–55.
- Marks, J.D., Hoogenboom, H.R., Bonnett, T.P., McCafferty, J., Griffiths, A.D. and Winter, G. (1991a) *J. Mol. Biol.*, **222**, 581–597.
- Marks, J.D., Tristram, M., Karpas, A. and Winter, G. (1991b) *Eur. J. Immunol.*, **21**, 985–991.
- Marks, J.D., Hoogenboom, H.R., Griffiths, A.D. and Winter, G. (1992a) *J. Biol. Chem.*, **267**, 16007–16010.
- Marks, J.D., Griffiths, A.D., Malmqvist, M., Clackson, T., Bye, J.M. and Winter, G. (1992b) *Bio/Technology*, **10**, 779–783.
- Masuda, H., Miller, C., Koeffler, H.P., Battifora, H. and Cline, M.J. (1987) *Proc. Natl Acad. Sci. USA*, **84**, 7716–7719.
- McCafferty, J., Griffiths, A.D., Winter, G. and Chiswell, D.J. (1990) *Nature*, **348**, 552–554.
- Merrick, W.C. (1979) *Methods Enzymol.*, **60**, 108–123.
- Midgely, C.A., Fisher, C.J., Bartek, J., Vojtesek, B., Lane, D. and Barnes, D.M. (1992) *J. Cell Sci.*, **101**, 183–189.
- Milstein, C. (1990) *Proc. R. Soc. Lond. Biol.*, **239**, 1–16.
- Munro, S. and Pelham, H.R.B. (1986) *Cell*, **46**, 291–300.
- Napier, R.M., Fowke, L.C., Hawes, C., Lewis, M. and Pelham, H.R.P. (1992) *J. Cell Sci.*, **102**, 261–271.
- Olden, K., Pratt, R.M., Jaworski, C. and Yamamda, K.M. (1979) *Proc. Natl Acad. Sci. USA*, **76**, 791–795.
- Orlandi, R., Gussow, D.H., Jones, P.T. and Winter, G. (1989) *Proc. Natl Acad. Sci. USA*, **86**, 3833–3837.
- Pack, P. and Pluckthun, A. (1992) *Biochemistry*, **31**, 1579–1584.
- Palter, K.B., Wanatabe, M., Stinson, L., Mahowald, A.P. and Craig, E.A. (1986) *Mol. Cell. Biol.*, **6**, 1187–1203.
- Pelham, H.R.B. (1989) *Annu. Rev. Cell Biol.*, **5**, 1–23.
- Perelson, A.S. and Oster, G.F. (1979) *J. Theor. Biol.*, **81**, 645–670.
- Pouyssegur, J., Shiu, R.P.C. and Pastan, I. (1977) *Cell*, **11**, 941–947.
- Saiki, R.K., Scharf, S., Faloona, F., Mullis, K.B., Horn, G.T., Erlich, H.A. and Arnheim, N. (1985) *Science*, **230**, 1350–1354.
- Sanger, F., Nicklen, S. and Coulson, A.R. (1977) *Proc. Natl Acad. Sci. USA*, **74**, 5463–5467.
- Sasso, E.H., Silverman, G.J. and Mannik, M. (1991) *J. Immunol.*, **147**, 1877–1883.
- Sastry, L., Altling, M.M., Huse, W.D., Short, J.M., Sorge, J.A., Hay, B.N., Janda, K.D., Benkovic, S.J. and Lerner, R.A. (1989) *Proc. Natl Acad. Sci. USA*, **86**, 5728–5732.
- Schlichtholz, B., Legros, Y., Gillet, D., Gaillard, C., Marty, M., Lane, D., Calvo, F. and Soussi, T. (1992) *Cancer Res.*, **52**, 6380–6384.
- Smith, G.P. (1985) *Science*, **228**, 1315–1317.
- Tomlinson, I.M., Walter, G., Marks, J.D., Llewellyn, M.B. and Winter, G. (1992) *J. Mol. Biol.*, **227**, 776–798.
- Towbin, H., Staehelin, R. and Gordon, J. (1979) *Proc. Natl Acad. Sci. USA*, **76**, 4350–4354.
- Vojtesek, B., Bartek, J., Midgely, C.A. and Lane, D.P. (1992) *J. Immunol. Methods*, **151**, 237–244.
- Ward, E.S., Gussow, D., Griffiths, A.D., Jones, P.T. and Winter, G. (1989) *Nature*, **341**, 544–546.
- Waterhouse, P., Griffiths, A.D., Johnson, K.S. and Winter, G. (1993) *Nucleic Acids Res.*, **21**, 2265–2266.
- Weber, S., Traunecker, A., Oliveri, F., Gerhard, W. and Karjalainen, K. (1992) *Nature*, **356**, 793–796.
- Winter, G. and Milstein, C. (1991) *Nature*, **349**, 293–299.
- Zouali, M. and Theze, J. (1991) *J. Immunol.*, **146**, 2855–2864.

Received on September 7, 1993